

## SEQUENCE LISTING

AP20 Rec'd PCT/PTO 26 MAY 2006

&lt;110&gt; Takeda Pharmaceutical Company Limited

&lt;120&gt; Method of Estimating Toxicity of Drug

&lt;130&gt; 09707

&lt;150&gt; JP 2003-397551

&lt;151&gt; 2003-11-27

&lt;160&gt; 60

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 4304

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (459).. (2033)

&lt;400&gt; 1

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Ala Gln Arg Ser Asp Leu Leu Glu Leu Asp Cys Gln Leu Thr Arg Asp  
5 10 15

aga gtg gtg gtg tca cat gat gag aac ctg tgc cgc cag tcg ggc 572  
Arg Val Val Val Val Ser His Asp Glu Asn Leu Cys Arg Gln Ser Gly  
20 25 30

cta aac agg gat gtg ggc agc ctg gac ttc gag gac ctg ccc ctc tac Leu Asn Arg Asp Val Gly Ser Leu Asp Phe Glu Asp Leu Pro Leu Tyr 35 40 45	620
aag gag aag ctg gag gtt tac ttc tct cca ggc cac ttt gct cac ggg Lys Glu Lys Leu Glu Val Tyr Phe Ser Pro Gly His Phe Ala His Gly 50 55 60 65	668
tca gac cgg cgc atg gtt cgt ctg gag gac ctg ttc cag agg ttt cca Ser Asp Arg Arg Met Val Arg Leu Glu Asp Leu Phe Gln Arg Phe Pro 70 75 80	716
agg aca ccc atg agc gta gag atc aaa ggg aag aac gaa gag ctc atc Arg Thr Pro Met Ser Val Glu Ile Lys Gly Lys Asn Glu Leu Ile 85 90 95	764
cgt gag ata gca ggc ttg gtg aga cgc tat gac cgt aat gaa atc acc Arg Glu Ile Ala Gly Leu Val Arg Arg Tyr Asp Arg Asn Glu Ile Thr 100 105 110	812
atc tgg gcc tcg gag aag agc tcg gtc atg aag aaa tgc aag gct gcc Ile Trp Ala Ser Glu Lys Ser Ser Val Met Lys Lys Cys Lys Ala Ala 115 120 125	860
aac ccc gag atg ccc ctg tcc ttc aca ata agc cga gga ttc tgg gtg Asn Pro Glu Met Pro Leu Ser Phe Thr Ile Ser Arg Gly Phe Trp Val 130 135 140 145	908
ctg ctt tcc tac tac ctg ggg ctg ctg ccc ttc atc cca atc cct gag Leu Leu Ser Tyr Tyr Leu Gly Leu Leu Pro Phe Ile Pro Ile Pro Glu 150 155 160	956
aag ttc ttc ttc tgc ttc ctg ccc aac atc atc aac agg acc tat ttc Lys Phe Phe Phe Cys Phe Leu Pro Asn Ile Ile Asn Arg Thr Tyr Phe 165 170 175	1004
cca ttt tcc tgc tct tgc ctg aac cag tta ttg gct gtg gtt tcg aaa Pro Phe Ser Cys Ser Cys Leu Asn Gln Leu Leu Ala Val Val Ser Lys 180 185 190	1052
tgg ctg atc atg agg aag agt ctg atc cga cac ttg gag gag cga ggg Trp Leu Ile Met Arg Lys Ser Leu Ile Arg His Leu Glu Glu Arg Gly 195 200 205	1100
gtg cag gtg gtc ttt tgg tgc ctt aat gaa gag tcg gat ttt gaa gca Val Gln Val Val Phe Trp Cys Leu Asn Glu Glu Ser Asp Phe Glu Ala 210 215 220 225	1148
gcc ttc agc gtg gga gcc act ggc gtc ata acg gat tat ccc aca gcc Ala Phe Ser Val Gly Ala Thr Gly Val Ile Thr Asp Tyr Pro Thr Ala 230 235 240	1196
ctg cgg cac tac ctg gac aac cat gga cca gct gcc cgg acc tcc Leu Arg His Tyr Leu Asp Asn His Gly Pro Ala Ala Arg Thr Ser 245 250 255	1241
taagtccaga agcctcgagg tcttctgttt ctcttctga aaaataaata ttgcctttc	1301
gatcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa	1336

<210> 6  
 <211> 256  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Met Ala Gln Arg Ser Asp Leu Leu Glu Leu Asp Cys Gln Leu Thr Arg  
1 5 10 15

Asp Arg Val Val Val Val Ser His Asp Glu Asn Leu Cys Arg Gln Ser  
20 25 30

Gly Leu Asn Arg Asp Val Gly Ser Leu Asp Phe Glu Asp Leu Pro Leu  
 35 40 45

Tyr Lys Glu Lys Leu Glu Val Tyr Phe Ser Pro Gly His Phe Ala His  
 50 55 60

Gly Ser Asp Arg Arg Met Val Arg Leu Glu Asp Leu Phe Gln Arg Phe  
 65 70 75 80

Pro Arg Thr Pro Met Ser Val Glu Ile Lys Gly Lys Asn Glu Glu Leu  
 85 90 95

Ile Arg Glu Ile Ala Gly Leu Val Arg Arg Tyr Asp Arg Asn Glu Ile  
 100 105 110

Thr Ile Trp Ala Ser Glu Lys Ser Ser Val Met Lys Lys Cys Lys Ala  
 115 120 125

Ala Asn Pro Glu Met Pro Leu Ser Phe Thr Ile Ser Arg Gly Phe Trp  
 130 135 140

Val Leu Leu Ser Tyr Tyr Leu Gly Leu Leu Pro Phe Ile Pro Ile Pro  
 145 150 155 160

Glu Lys Phe Phe Phe Cys Phe Leu Pro Asn Ile Ile Asn Arg Thr Tyr  
 165 170 175

Phe Pro Phe Ser Cys Ser Cys Leu Asn Gln Leu Leu Ala Val Val Ser  
 180 185 190

Lys Trp Leu Ile Met Arg Lys Ser Leu Ile Arg His Leu Glu Glu Arg  
 195 200 205

Gly Val Gln Val Val Phe Trp Cys Leu Asn Glu Glu Ser Asp Phe Glu  
 210 215 220

Ala Ala Phe Ser Val Gly Ala Thr Gly Val Ile Thr Asp Tyr Pro Thr  
 225 230 235 240

Ala Leu Arg His Tyr Leu Asp Asn His Gly Pro Ala Ala Arg Thr Ser  
 245 250 255

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 <211> 2631  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (19).. (2214)

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 Met Thr Glu Gly Thr Cys Leu Arg Arg Arg Gly  
 1 5 10

ggc ccc tac aag acc gag ccc gcc acc gac ctc ggc cgc tgg cga ctc 99  
 Gly Pro Tyr Lys Thr Glu Pro Ala Thr Asp Leu Gly Arg Trp Arg Leu  
 15 20 25

aac tgc gag agg ggc cgg cag acg tgg acc tac ctg cag gac gag cgc Asn Cys Glu Arg Gly Arg Gln Thr Trp Thr Tyr Leu Gln Asp Glu Arg 30 35 40	147
gcc ggc cgc gag cag acc ggc ctg gaa gcc tac gcc ctg ggg ctg gac Ala Gly Arg Glu Gln Thr Gly Leu Glu Ala Tyr Ala Leu Gly Leu Asp 45 50 55	195
acc aag aat tac ttt aag gac ttg ccc aaa gcc cac acc gcc ttt gag Thr Lys Asn Tyr Phe Lys Asp Leu Pro Lys Ala His Thr Ala Phe Glu 60 65 70 75	243
ggg gct ctg aac ggc atg aca ttt tac gtg ggg ctg cag gct gag gat Gly Ala Leu Asn Gly Met Thr Phe Tyr Val Gly Leu Gln Ala Glu Asp 80 85 90	291
ggg cac tgg acg ggt gat tat ggt ggc cca ctt ttc ctc ctg cca ggc Gly His Trp Thr Gly Asp Tyr Gly Thr Pro Leu Phe Leu Leu Pro Gly 95 100 105	339
ctc ctg atc act tgc cac gtg gca cgc atc cct ctg cca gcc gga tac Leu Leu Ile Thr Cys His Val Ala Arg Ile Pro Leu Pro Ala Gly Tyr 110 115 120	387
aga gaa gag att gtg cgg tac ctg cgg tca gtg cag ctc cct gac ggt Arg Glu Glu Ile Val Arg Tyr Leu Arg Ser Val Gln Leu Pro Asp Gly 125 130 135	435
ggc tgg ggc ctg cac att gag gat aag tcc acc gtg ttt ggg act gcg Gly Trp Gly Leu His Ile Glu Asp Lys Ser Thr Val Phe Gly Thr Ala 140 145 150 155	483
ctc aac tat gtg tct ctc aga att ctg ggt gtt ggg cct gac gat cct Leu Asn Tyr Val Ser Leu Arg Ile Leu Gly Val Gly Pro Asp Asp Pro 160 165 170	531
gac ctg gta cga gcc cgg aac att ctt cac aag aaa ggt ggt gct gtg Asp Leu Val Arg Ala Arg Asn Ile Leu His Lys Lys Gly Gly Ala Val 175 180 185	579
gcc atc ccc tcc tgg ggg aag ttc tgg ctg gct gtc ctg aat gtt tac Ala Ile Pro Ser Trp Gly Lys Phe Trp Leu Ala Val Leu Asn Val Tyr 190 195 200	627
agc tgg gaa ggc ctc aat acc ctg ttc cca gag atg tgg ctg ttt cct Ser Trp Glu Gly Leu Asn Thr Leu Phe Pro Glu Met Trp Leu Phe Pro 205 210 215	675
gac tgg gca ccg gca cac ccc tcc aca ctc tgg tgc cac tgc cgg cag Asp Trp Ala Pro Ala His Pro Ser Thr Leu Trp Cys His Cys Arg Gln 220 225 230 235	723
gtg tac ctg ccc atg agc tac tgc tac gcc gtt cgg ctg agt gcc gcg Val Tyr Leu Pro Met Ser Tyr Cys Tyr Ala Val Arg Leu Ser Ala Ala 240 245 250	771
gaa gac ccg ctg gtc cag agc ctc cgc cag gag ctc tat gtg gag gac Glu Asp Pro Leu Val Gln Ser Leu Arg Gln Glu Leu Tyr Val Glu Asp 255 260 265	819
ttc gcc agc att gac tgg ctg gcg cag agg aac aac gtg gcc ccc gac Phe Ala Ser Ile Asp Trp Leu Ala Gln Arg Asn Asn Val Ala Pro Asp 270 275 280	867
gag ctg tac acg ccg cac agc tgg ctg ctc cgc gtg gta tat gcg ctc Glu Leu Tyr Thr Pro His Ser Trp Leu Leu Arg Val Val Tyr Ala Leu 285 290 295	915
ctc aac ctg tat gag cac cac cac agt gcc cac ctg cgg cag cgg gcc Leu Asn Leu Tyr Glu His His His Ser Ala His Leu Arg Gln Arg Ala 300 305 310 315	963
gtg cag aag ctg tat gaa cac att gtg gcc gac gac cga ttc acc aag Val Gln Lys Leu Tyr Glu His Ile Val Ala Asp Asp Arg Phe Thr Lys 320 325 330	1011

agc atc agc atc ggc ccg atc tcg aaa acc atc aac atg ctt gtg cgc Ser Ile Ser Ile Gly Pro Ile Ser Lys Thr Ile Asn Met Leu Val Arg 335 340 345	1059
tgg tat gtg gac ggg ccc gcc tcc act gcc ttc cag gag cat gtc tcc Trp Tyr Val Asp Gly Pro Ala Ser Thr Ala Phe Gln Glu His Val Ser 350 355 360	1107
aga atc ccg gac tat ctc tgg atg ggc ctt gac ggc atg aaa atg cag Arg Ile Pro Asp Tyr Leu Trp Met Gly Leu Asp Gly Met Lys Met Gln 365 370 375	1155
ggc acc aac ggc tca cag atc tgg gac acc gca ttc gcc atc cag gct Gly Thr Asn Gly Ser Gln Ile Trp Asp Thr Ala Phe Ala Ile Gln Ala 380 385 390 395	1203
ctg ctt gag ggc ggc ggg cac cac agg ccc gag ttt tcg tcc tgc ctg Leu Leu Glu Ala Gly Gly His His Arg Pro Glu Phe Ser Ser Cys Leu 400 405 410	1251
cag aag gct cat gag ttc ctg agg ctc tca cag gtc cca gat aac cct Gln Lys Ala His Glu Phe Leu Arg Leu Ser Gln Val Pro Asp Asn Pro 415 420 425	1299
ccc gac tac cag aag tac tac cgc cag atg cgc aag ggt ggc ttc tcc Pro Asp Tyr Gln Lys Tyr Tyr Arg Gln Met Arg Lys Gly Gly Phe Ser 430 435 440	1347
ttc agt acg ctg gac tgc ggc tgg atc gtt tct gac tgc acg gct gag Phe Ser Thr Leu Asp Cys Gly Trp Ile Val Ser Asp Cys Thr Ala Glu 445 450 455	1395
gcc ttg aag gct gtg ctg ctc ctg cag gag aag tgt ccc cat gtc acc Ala Leu Lys Ala Val Leu Leu Gln Glu Lys Cys Pro His Val Thr 460 465 470 475	1443
gag cac atc ccc aga gaa cgg ctc tgc gat got gtg gct gtg ctg ctg Glu His Ile Pro Arg Glu Arg Leu Cys Asp Ala Val Ala Val Leu Leu 480 485 490	1491
aac atg aga aat cca gat gga ggg ttc gcc acc tat gag acc aag cgt Asn Met Arg Asn Pro Asp Gly Gly Phe Ala Thr Tyr Glu Thr Lys Arg 495 500 505	1539
ggg ggg cac ttg ctg gag ctg ctg aac ccc tcg gag gtc ttc ggg gac Gly Gly His Leu Leu Glu Leu Leu Asn Pro Ser Glu Val Phe Gly Asp 510 515 520	1587
atc atg att gac tac acc tat gtg gag tgc acc tca gcc gtg atg cag Ile Met Ile Asp Tyr Thr Tyr Val Glu Cys Thr Ser Ala Val Met Gln 525 530 535	1635
gcg ctt aag tat ttc cac aag cgt ttc ccg gag cac agg gca gcg gag Ala Leu Lys Tyr Phe His Lys Arg Phe Pro Glu His Arg Ala Ala Glu 540 545 550 555	1683
atc cgg gag acc ctc acg cag ggc tta gag ttc tgt cgg cgg cag cag Ile Arg Glu Thr Leu Thr Gln Gly Leu Glu Phe Cys Arg Arg Gln Gln 560 565 570	1731
agg gcc gat ggc tcc tgg gaa ggc tcc tgg gga gtt tgc ttc acc tac Arg Ala Asp Gly Ser Trp Glu Gly Ser Trp Gly Val Cys Phe Thr Tyr 575 580 585	1779
ggc acc tgg ttt ggc ctg gag gcc ttc gcc tgt atg ggg cag acc tac Gly Thr Trp Phe Gly Leu Glu Ala Phe Ala Cys Met Gly Gln Thr Tyr 590 595 600	1827
cga gat ggg act gcc tgt gca gag gtc tcc ccg gcc tgt gac ttc ctg Arg Asp Gly Thr Ala Cys Ala Glu Val Ser Arg Ala Cys Asp Phe Leu 605 610 615	1875
ctg tcc cgg cag atg gca gac gga ggc tgg ggg gag gac ttt gag tcc Leu Ser Arg Gln Met Ala Asp Gly Gly Trp Gly Glu Asp Phe Glu Ser 620 625 630 635	1923

tgc gag gag cgg cgt tat ttg cag agt gcc cag tcc cag atc cat aac Cys Glu Glu Arg Arg Tyr Leu Gln Ser Ala Gln Ser Gln Ile His Asn 640 645 650	1971
aca tgc tgg gcc atg atg ggg ctg atg gcc gtt cgg cat cct gac atc Thr Cys Trp Ala Met Met Gly Leu Met Ala Val Arg His Pro Asp Ile 655 660 665	2019
gag gcc cag gag aga gga gtc cgg tgt cta ctt gag aaa cag ctc ccc Glu Ala Gln Glu Arg Gly Val Arg Cys Leu Leu Glu Lys Gln Leu Pro 670 675 680	2067
aat ggc gac tgg cgg cag gaa aac att gct ggg gtc ttc aac aag tcc Asn Gly Asp Trp Pro Gln Glu Asn Ile Ala Gly Val Phe Asn Lys Ser 685 690 695	2115
tgt gcc atc tcc tac acg agc tac agg aac atc ttc ccc atc tgg gcc Cys Ala Ile Ser Tyr Thr Ser Tyr Arg Asn Ile Phe Pro Ile Trp Ala 700 705 710 715	2163
ctc ggc cgc ttc tcc cag ctg tac cct gag aga gcc ctt gct ggc cac Leu Gly Arg Phe Ser Gln Leu Tyr Pro Glu Arg Ala Leu Ala Gly His 720 725 730	2211
ccc tgagaacatg cctacctgct gggcgccgtc tgtgcgttcc atggccttca Pro	2264
agtcacagga cgcagcgatt ccctgccctc ttcggtgtta ttacacaggc aggacttcag	2324
tgtcagtatc cctgccttca gtcttcttta gaaatcacat ctgtgttcaa tccattgttt	2384
agagggagtg tatttttccct gtccacgaa gaggactttt tgttcacaat tggatcacia	2444
tgcagaggag tctgttccct ccccgctggc ttctcggtgc tgggagggtg acctgtccca	2504
gatgactcat caccctgaca tgctcttgac aaaggacacc accaagagga gatggcagct	2564
gtaccggtgc agcctctgtc tgagggggat attgcctca gtgtgattaa aaatcagtca	2624
tgaaaga	2631

<210> 8  
 <211> 732  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Met Thr Glu Gly Thr Cys Leu Arg Arg Arg Gly Gly Pro Tyr Lys Thr  
 1 5 10 15

Glu Pro Ala Thr Asp Leu Gly Arg Trp Arg Leu Asn Cys Glu Arg Gly  
 20 25 30

Arg Gln Thr Trp Thr Tyr Leu Gln Asp Glu Arg Ala Gly Arg Glu Gln  
 35 40 45

Thr Gly Leu Glu Ala Tyr Ala Leu Gly Leu Asp Thr Lys Asn Tyr Phe  
 50 55 60

Lys Asp Leu Pro Lys Ala His Thr Ala Phe Glu Gly Ala Leu Asn Gly  
 65 70 75 80

Met Thr Phe Tyr Val Gly Leu Gln Ala Glu Asp Gly His Trp Thr Gly  
 85 90 95

Asp Tyr Gly Gly Pro Leu Phe Leu Leu Pro Gly Leu Leu Ile Thr Cys  
 100 105 110

His Val Ala Arg Ile Pro Leu Pro Ala Gly Tyr Arg Glu Glu Ile Val  
115 120 125

Arg Tyr Leu Arg Ser Val Gln Leu Pro Asp Gly Gly Trp Gly Leu His  
130 135 140

Ile Glu Asp Lys Ser Thr Val Phe Gly Thr Ala Leu Asn Tyr Val Ser  
145 150 155 160

Leu Arg Ile Leu Gly Val Gly Pro Asp Asp Pro Asp Leu Val Arg Ala  
165 170 175

Arg Asn Ile Leu His Lys Lys Gly Gly Ala Val Ala Ile Pro Ser Trp  
180 185 190

Gly Lys Phe Trp Leu Ala Val Leu Asn Val Tyr Ser Trp Glu Gly Leu  
195 200 205

Asn Thr Leu Phe Pro Glu Met Trp Leu Phe Pro Asp Trp Ala Pro Ala  
210 215 220

His Pro Ser Thr Leu Trp Cys His Cys Arg Gln Val Tyr Leu Pro Met  
225 230 235 240

Ser Tyr Cys Tyr Ala Val Arg Leu Ser Ala Ala Glu Asp Pro Leu Val  
245 250 255

Gln Ser Leu Arg Gln Glu Leu Tyr Val Glu Asp Phe Ala Ser Ile Asp  
260 265 270

Trp Leu Ala Gln Arg Asn Asn Val Ala Pro Asp Glu Leu Tyr Thr Pro  
275 280 285

His Ser Trp Leu Leu Arg Val Val Tyr Ala Leu Leu Asn Leu Tyr Glu  
290 295 300

His His His Ser Ala His Leu Arg Gln Arg Ala Val Gln Lys Leu Tyr  
305 310 315 320

Glu His Ile Val Ala Asp Asp Arg Phe Thr Lys Ser Ile Ser Ile Gly  
325 330 335

Pro Ile Ser Lys Thr Ile Asn Met Leu Val Arg Trp Tyr Val Asp Gly  
340 345 350

Pro Ala Ser Thr Ala Phe Gln Glu His Val Ser Arg Ile Pro Asp Tyr  
355 360 365

Leu Trp Met Gly Leu Asp Gly Met Lys Met Gln Gly Thr Asn Gly Ser  
370 375 380

Gln Ile Trp Asp Thr Ala Phe Ala Ile Gln Ala Leu Leu Glu Ala Gly  
385 390 395 400

Gly His His Arg Pro Glu Phe Ser Ser Cys Leu Gln Lys Ala His Glu  
405 410 415

Phe Leu Arg Leu Ser Gln Val Pro Asp Asn Pro Pro Asp Tyr Gln Lys  
 420 425 430  
 Tyr Tyr Arg Gln Met Arg Lys Gly Gly Phe Ser Phe Ser Thr Leu Asp  
 435 440 445  
 Cys Gly Trp Ile Val Ser Asp Cys Thr Ala Glu Ala Leu Lys Ala Val  
 450 455 460  
 Leu Leu Leu Gln Glu Lys Cys Pro His Val Thr Glu His Ile Pro Arg  
 465 470 475 480  
 Glu Arg Leu Cys Asp Ala Val Ala Val Leu Leu Asn Met Arg Asn Pro  
 485 490 495  
 Asp Gly Gly Phe Ala Thr Tyr Glu Thr Lys Arg Gly Gly His Leu Leu  
 500 505 510  
 Glu Leu Leu Asn Pro Ser Glu Val Phe Gly Asp Ile Met Ile Asp Tyr  
 515 520 525  
 Thr Tyr Val Glu Cys Thr Ser Ala Val Met Gln Ala Leu Lys Tyr Phe  
 530 535 540  
 His Lys Arg Phe Pro Glu His Arg Ala Ala Glu Ile Arg Glu Thr Leu  
 545 550 555 560  
 Thr Gln Gly Leu Glu Phe Cys Arg Arg Gln Gln Arg Ala Asp Gly Ser  
 565 570 575  
 Trp Glu Gly Ser Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly  
 580 585 590  
 Leu Glu Ala Phe Ala Cys Met Gly Gln Thr Tyr Arg Asp Gly Thr Ala  
 595 600 605  
 Cys Ala Glu Val Ser Arg Ala Cys Asp Phe Leu Leu Ser Arg Gln Met  
 610 615 620  
 Ala Asp Gly Gly Trp Gly Glu Asp Phe Glu Ser Cys Glu Glu Arg Arg  
 625 630 635 640  
 Tyr Leu Gln Ser Ala Gln Ser Gln Ile His Asn Thr Cys Trp Ala Met  
 645 650 655  
 Met Gly Leu Met Ala Val Arg His Pro Asp Ile Glu Ala Gln Glu Arg  
 660 665 670  
 Gly Val Arg Cys Leu Leu Glu Lys Gln Leu Pro Asn Gly Asp Trp Pro  
 675 680 685  
 Gln Glu Asn Ile Ala Gly Val Phe Asn Lys Ser Cys Ala Ile Ser Tyr  
 690 695 700  
 Thr Ser Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Arg Phe Ser  
 705 710 715 720



Gln Leu Tyr Pro Glu Arg Ala Leu Ala Gly His Pro  
725 730

<210> 9  
<211> 1168  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (30).. (800)

<400> 9  
gagctggaag tgagagcaga tccctaacc atg agc acc agc caa cca ggg gcc 53  
Met Ser Thr Ser Gln Pro Gly Ala  
1 5

tgc cca tgc cag gga gct gca agc cgc ccc gcc att ctc tac gca ctt 101  
Cys Pro Cys Gln Gly Ala Ala Ser Arg Pro Ala Ile Leu Tyr Ala Leu  
10 15 20

ctg agc tcc agc ctc aag gct gtc ccc cga ccc cgt agc cgc tgc cta 149  
Leu Ser Ser Ser Leu Lys Ala Val Pro Arg Pro Arg Ser Arg Cys Leu  
25 30 35 40

tgt agg cag cac cgg ccc gtc cag cta tgt gca cct cat cgc acc tgc 197  
Cys Arg Gln His Arg Pro Val Gln Leu Cys Ala Pro His Arg Thr Cys  
45 50 55

cgg gag gcc ttg gat gtt ctg gcc aag aca gtg gcc ttc ctc agg aac 245  
Arg Glu Ala Leu Asp Val Leu Ala Lys Thr Val Ala Phe Leu Arg Asn  
60 65 70

ctg cca tcc ttc tgg cag ctg cct ccc cag gac cag cgg cgg ctg ctg 293  
Leu Pro Ser Phe Trp Gln Leu Pro Pro Gln Asp Gln Arg Arg Leu Leu  
75 80 85

cag ggt tgc tgg ggc ccc ctc ttc ctg ott ggg ttg gcc caa gat gct 341  
Gln Gly Cys Trp Gly Pro Leu Phe Leu Leu Gly Leu Ala Gln Asp Ala  
90 95 100

gtg acc ttt gag gtg gct gag gcc cgg gtg ccc agc ata ctc aag aag 389  
Val Thr Phe Glu Val Ala Glu Ala Pro Val Pro Ser Ile Leu Lys Lys  
105 110 115 120

att ctg ctg gag gag ccc agc agc agt gga ggc agt ggc caa ctg cca 437  
Ile Leu Leu Glu Glu Pro Ser Ser Ser Gly Gly Ser Gly Gln Leu Pro  
125 130 135

gac aga ccc cag ccc tcc ctg gct gcg gtg cag tgg ctt caa tgc tgt 485  
Asp Arg Pro Gln Pro Ser Leu Ala Ala Val Gln Trp Leu Gln Cys Cys  
140 145 150

ctg gag tcc ttc tgg agc ctg gag ott agc ccc aag gaa tat gcc tgc 533  
Leu Glu Ser Phe Trp Ser Leu Glu Leu Ser Pro Lys Glu Tyr Ala Cys  
155 160 165

ctg aaa ggg acc atc ctc ttc aac ccc gat gtg cca ggc ctc caa gcc 581  
Leu Lys Gly Thr Ile Leu Phe Asn Pro Asp Val Pro Gly Leu Gln Ala  
170 175 180

gcc tcc cac att ggg cac ctg cag cag gag gct cac tgg gtg ctg tgt 629  
Ala Ser His Ile Gly His Leu Gln Gln Glu Ala His Trp Val Leu Cys  
185 190 195 200

gaa gtc ctg gaa ccc tgg tgc cca gca gcc caa ggc cgc ctg acc cgt 677  
Glu Val Leu Glu Pro Trp Cys Pro Ala Ala Gln Gly Arg Leu Thr Arg  
205 210 215

gtc ctc ctc acg gcc tcc acc ctc aag tcc att ccg acc agc ctg ctt 725  
Val Leu Leu Thr Ala Ser Thr Leu Lys Ser Ile Pro Thr Ser Leu Leu  
220 225 230

ggg gac ctc ttc ttt cgc cct atc att gga gat gtt gac atc gct ggc 773  
 Gly Asp Leu Phe Phe Arg Pro Ile Ile Gly Asp Val Asp Ile Ala Gly  
 235 240 245  
 ctt ctt ggg gac atg ctt ttg ctc agg tgacctgttc cagcccaggc 820  
 Leu Leu Gly Asp Met Leu Leu Leu Arg  
 250 255  
 agagatcagg tgggcagagg ctggcagtcg tgattcagcc tggccatccc cagaggtgac 880  
 ccaatgctcc tggaggggca agcctgtata gacagcactt ggctccttag gaacagctct 940  
 tcactcagcc acaccccaca ttggaattcc ttggtttgga cacagtgtc cagctgcctg 1000  
 ggaggctttt ggtggtcccc acagcctctg ggccaagact cctgtccctt cttgggatga 1060  
 gaatgaaagc ttaggctgct tattggacca gaagtcctat cgactttata cagaactgaa 1120  
 ttaagttatt gatttttgta ataaaagta tgaacacta aaaaaaaaa 1168

<210> 10  
 <211> 257  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Met Ser Thr Ser Gln Pro Gly Ala Cys Pro Cys Gln Gly Ala Ala Ser  
 1 5 10 15  
 Arg Pro Ala Ile Leu Tyr Ala Leu Leu Ser Ser Ser Leu Lys Ala Val  
 20 25 30  
 Pro Arg Pro Arg Ser Arg Cys Leu Cys Arg Gln His Arg Pro Val Gln  
 35 40 45  
 Leu Cys Ala Pro His Arg Thr Cys Arg Glu Ala Leu Asp Val Leu Ala  
 50 55 60  
 Lys Thr Val Ala Phe Leu Arg Asn Leu Pro Ser Phe Trp Gln Leu Pro  
 65 70 75 80  
 Pro Gln Asp Gln Arg Arg Leu Leu Gln Gly Cys Trp Gly Pro Leu Phe  
 85 90 95  
 Leu Leu Gly Leu Ala Gln Asp Ala Val Thr Phe Glu Val Ala Glu Ala  
 100 105 110  
 Pro Val Pro Ser Ile Leu Lys Lys Ile Leu Leu Glu Glu Pro Ser Ser  
 115 120 125  
 Ser Gly Gly Ser Gly Gln Leu Pro Asp Arg Pro Gln Pro Ser Leu Ala  
 130 135 140  
 Ala Val Gln Trp Leu Gln Cys Cys Leu Glu Ser Phe Trp Ser Leu Glu  
 145 150 155 160  
 Leu Ser Pro Lys Glu Tyr Ala Cys Leu Lys Gly Thr Ile Leu Phe Asn  
 165 170 175  
 Pro Asp Val Pro Gly Leu Gln Ala Ala Ser His Ile Gly His Leu Gln  
 180 185 190

Gln Glu Ala His Trp Val Leu Cys Glu Val Leu Glu Pro Trp Cys Pro  
195 200 205

Ala Ala Gln Gly Arg Leu Thr Arg Val Leu Leu Thr Ala Ser Thr Leu  
210 215 220

Lys Ser Ile Pro Thr Ser Leu Leu Gly Asp Leu Phe Phe Arg Pro Ile  
225 230 235 240

Ile Gly Asp Val Asp Ile Ala Gly Leu Leu Gly Asp Met Leu Leu Leu  
245 250 255

Arg

<210> 11  
<211> 489  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (43).. (423)

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Met Ser Phe Ser  
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ggc aag tac caa ctg cag agc cag gaa aac ttt gaa gcc ttc atg aag 102  
Gly Lys Tyr Gln Leu Gln Ser Gln Glu Asn Phe Glu Ala Phe Met Lys  
5 10 15 20

gca atc ggt ctg ccg gaa gag ctc atc cag aag ggg aag gat atc aag 150  
Ala Ile Gly Leu Pro Glu Glu Leu Ile Gln Lys Gly Lys Asp Ile Lys  
25 30 35

ggg gtg tcg gaa atc gtg cag aat ggg aag cac ttc aag ttc acc atc 198  
Gly Val Ser Glu Ile Val Gln Asn Gly Lys His Phe Lys Phe Thr Ile  
40 45 50

acc gct ggg tcc aaa gtg atc caa aac gaa ttc acg gtg ggg gag gaa 246  
Thr Ala Gly Ser Lys Val Ile Gln Asn Glu Phe Thr Val Gly Glu Glu  
55 60 65

tgt gag ctg gag aca atg aca ggg gag aaa gtc aag aca gtg gtt cag 294  
Cys Glu Leu Glu Thr Met Thr Gly Glu Lys Val Lys Thr Val Val Gln  
70 75 80

ttg gaa ggt gac aat aaa ctg gtg aca act ttc aaa aac atc aag tct 342  
Leu Glu Gly Asp Asn Lys Leu Val Thr Thr Phe Lys Asn Ile Lys Ser  
85 90 95 100

gtg acc gaa ctc aac ggc gac ata atc acc aat acc atg aca ttg ggt 390  
Val Thr Glu Leu Asn Gly Asp Ile Ile Thr Asn Thr Met Thr Leu Gly  
105 110 115

gac att gtc ttc aag aga atc agc aag aga att taaacaagtc tgcatttcac 443  
Asp Ile Val Phe Lys Arg Ile Ser Lys Arg Ile  
120 125

attatttttag tgtgtaaaat taatgtaata aagtgaactt tgtttt 489

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<213> Homo sapiens

<400> 12

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Ala Phe Met Lys Ala Ile Gly Leu Pro Glu Glu Leu Ile Gln Lys Gly  
20 25 30

Lys Asp Ile Lys Gly Val Ser Glu Ile Val Gln Asn Gly Lys His Phe  
35 40 45

Lys Phe Thr Ile Thr Ala Gly Ser Lys Val Ile Gln Asn Glu Phe Thr  
50 55 60

Val Gly Glu Glu Cys Glu Leu Glu Thr Met Thr Gly Glu Lys Val Lys  
65 70 75 80

Thr Val Val Gln Leu Glu Gly Asp Asn Lys Leu Val Thr Thr Phe Lys  
85 90 95

Asn Ile Lys Ser Val Thr Glu Leu Asn Gly Asp Ile Ile Thr Asn Thr  
100 105 110

Met Thr Leu Gly Asp Ile Val Phe Lys Arg Ile Ser Lys Arg Ile  
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tgcccaggcc tggagactga cccgaccccg gcactacctc gaggtccgc cccacactgc 180

tggaccccag ggtcccaccc tggcccagga ggtcagccag ggaatcatta acaagaggca 240

gtgac atg gcg cag aag gag ggt ggc cgg act gtg cca tgc tgc tcc 287  
Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser  
-160 -155 -150

aga ccc aag gtg gca gct ctc act gcg ggg acc ctg cta ott ctg 332  
Arg Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu  
-145 -140 -135

aca gcc atc ggg gcg gca tcc tgg gcc att gtg gct gtt ctc ctc 377  
Thr Ala Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu  
-130 -125 -120

agg agt gac cag gag ccg ctg tac cca gtg cag gtc agc tct gcg 422  
Arg Ser Asp Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala  
-115 -110 -105

(20)

gac gct cgg ctc atg gtc ttt gac aag acg gaa ggg acg tgg cgg ctg Asp Ala Arg Leu Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu -100 -95 -90	470
ctg tgc tcc tgc cgc tcc aac gcc agg gta gcc gga ctc agc tgc gag Leu Cys Ser Ser Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu -85 -80 -75	518
gag atg ggc ttc ctc agg gca ctg acc cac tcc gag ctg gac gtg cga Glu Met Gly Phe Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg -70 -65 -60	566
acg gcg ggc gcc aat ggc acg tgc ggc ttc ttc tgt gtg gac gag ggg Thr Ala Gly Ala Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly -55 -50 -45 -40	614
agg ctg ccc cac acc cag agg ctg ctg gag gtc atc tcc gtg tgt gat Arg Leu Pro His Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp -35 -30 -25	662
tgc ccc aga ggc cgt ttc ttg gcc gcc atc tgc caa gac tgt ggc cgc Cys Pro Arg Gly Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg -20 -15 -10	710
agg aag ctg ccc gtg gac cgc atc gtg gga ggc cgg gac acc agc ttg Arg Lys Leu Pro Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu -5 -1 1 5	758
ggc cgg tgg cgg tgg caa gtc agc ctt cgc tat gat gga gca cac ctc Gly Arg Trp Pro Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu 10 15 20 25	806
tgt ggg gga tcc ctg ctc tcc ggg gac tgg gtg ctg aca gcc gcc cac Cys Gly Gly Ser Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His 30 35 40	854
tgc ttc cgg gag cgg aac cgg gtc ctg tcc cga tgg cga gtg ttt gcc Cys Phe Pro Glu Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala 45 50 55	902
ggt gcc gtg gcc cag gcc tct ccc cac ggt ctg cag ctg ggg gtg cag Gly Ala Val Ala Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln 60 65 70	950
gct gtg gtc tac cac ggc ggc tat ctt ccc ttt cgg gac ccc aac agc Ala Val Val Tyr His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser 75 80 85	998
gag gag aac agc aac gat att gcc ctg gtc cac ctc tcc agt ccc ctg Glu Glu Asn Ser Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu 90 95 100 105	1046
ccc ctc aca gaa tac atc cag cct gtg tgc ctc cca gct gcc ggc cag Pro Leu Thr Glu Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln 110 115 120	1094
gcc ctg gtg gat ggc aag atc tgt acc gtg acg ggc tgg ggc aac acg Ala Leu Val Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr 125 130 135	1142
cag tac tat ggc caa cag gcc ggg gta ctc cag gag gct cga gtc ccc Gln Tyr Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro 140 145 150	1190
ata atc agc aat gat gtc tgc aat ggc gct gac ttc tat gga aac cag Ile Ile Ser Asn Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln 155 160 165	1238
atc aag ccc aag atg ttc tgt gct ggc tac ccc gag ggt ggc att gat Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp 170 175 180 185	1286
gcc tgc cag ggc gac agc ggt ggt ccc ttt gtg tgt gag gac agc atc Ala Cys Gln Gly Asp Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile 190 195 200	1334

tct cgg acg cca cgt tgg cgg ctg tgt ggc att gtg agt tgg ggc act	1382
Ser Arg Thr Pro Arg Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr	
205 210 215	
ggc tgt gcc ctg gcc cag aag cca ggc gtc tac acc aaa gtc agt gac	1430
Gly Cys Ala Leu Ala Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp	
220 225 230	
ttc cgg gag tgg atc ttc cag gcc ata aag act cac tcc gaa gcc agc	1478
Phe Arg Glu Trp Ile Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser	
235 240 245	
ggc atg gtg acc cag ctc tgaccggtgg ctctctgctg cgcagcctcc	1526
Gly Met Val Thr Gln Leu	
250 255	
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tcttgggccc ggtccacagg tccaaggaca ccctccctcc agggtcctct cttccacagt	1646
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taaagatggt ttgtatt	1783

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 <213> Homo sapiens

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Ala Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg	
-130 -125 -120	
Ser Asp Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp	
-115 -110 -105	
Ala Arg Leu Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu	
-100 -95 -90	
Cys Ser Ser Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu	
-85 -80 -75	
Met Gly Phe Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr	
-70 -65 -60 -55	
Ala Gly Ala Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg	
-50 -45 -40	
Leu Pro His Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys	
-35 -30 -25	
Pro Arg Gly Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg	
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 Leu Gly Leu Leu Ala Ala Gly Phe Cys Pro Ala Val Leu Cys His Pro  
 -15 -10 -5 -1

aac agc cca ctt gac gag gag aat ctg acc cag gag aac caa gac cga 148  
 Asn Ser Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg  
 1 5 10 15

ggg aca cac gtg gac ctc gga tta gcc tcc gcc aac gtg gac ttc gct 196  
 Gly Thr His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala  
 20 25 30

ttc agc ctg tac aag cag tta gtc ctg aag gcc ctt gat aag aat gtc 244  
 Phe Ser Leu Tyr Lys Gln Leu Val Leu Lys Ala Leu Asp Lys Asn Val  
 35 40 45

atc ttc tcc cca ctg agc atc tcc acc gcc ttg gcc ttc ctg tct ctg 292  
 Ile Phe Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu  
 50 55 60

ggg gcc cat aat acc acc ctg aca gag att ctc aag gcc tcg agt tca 340  
 Gly Ala His Asn Thr Thr Leu Thr Glu Ile Leu Lys Ala Ser Ser Ser  
 65 70 75 80

cct cac gga gac tta ctg agg cag aaa ttc act cag agc ttc cag cac 388  
 Pro His Gly Asp Leu Leu Arg Gln Lys Phe Thr Gln Ser Phe Gln His  
 85 90 95

ctc cgc gca ccc tca atc agt tcc agc gat gag ctg cag ctg agt atg 436  
 Leu Arg Ala Pro Ser Ile Ser Ser Ser Asp Glu Leu Gln Leu Ser Met  
 100 105 110

gga aat gcc atg ttt gtc aaa gag caa ctc agt ctg ctg gac agg ttc 484  
 Gly Asn Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe  
 115 120 125

acg gag gat gcc aag agg ctg tat ggc tcc gag gcc ttt gcc act gac 532  
 Thr Glu Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp  
 130 135 140

ttt cag gac tca gct gca gct aag aag ctc atc aac gac tac gtg aag 580  
 Phe Gln Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys  
 145 150 155 160

aat gga act agg ggg aaa atc aca gat ctg atc aag gac ccc gac tcg 628  
 Asn Gly Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Pro Asp Ser  
 165 170 175

cag aca atg atg gtc ctg gtg aat tac atc ttc ttt aaa gcc aaa tgg 676  
 Gln Thr Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp  
 180 185 190

gag atg ccc ttt gac ccc caa gat act cat cag tca agg ttc tac ttg 724  
 Glu Met Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu  
 195 200 205

agc aag aaa aag tgg gta atg gtg ccc atg atg agt ttg cat cac ctg 772  
 Ser Lys Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu  
 210 215 220

act ata cct tac ttc cgg gac gag gag ctg tcc tgc acc gtg gtg gag 820  
 Thr Ile Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu



225	230	235	240	
ctg aag tac aca ggc aat gcc agc gca ctc ttc atc ctc cct gat caa Leu Lys Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln 245 250 255				868
gac aag atg gag gaa gtg gaa gcc atg ctg ctc cca gag acc ctg aag Asp Lys Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys 260 265 270				916
cgg tgg aga gac tct ctg gag ttc aga gag ata ggt gag ctc tac ctg Arg Trp Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu 275 280 285				964
cca aag ttt tcc atc tcg agg gac tat aac ctg aac gac ata ctt ctc Pro Lys Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu 290 295 300				1012
cag ctg ggc att gag gaa gcc ttc acc agc aag gct gac ctg tca ggg Gln Leu Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly 305 310 315 320				1060
atc aca ggg gcc agg aac cta gca gtc tcc cag gtg gtc cat aag gtc Ile Thr Gly Ala Arg Asn Leu Ala Val Thr Ser Gln Val Val His Lys Val 325 330 335				1108
gtg tct gat gta ttt gag gag ggc aca gaa gca tct gct gcc aca gca Val Ser Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala 340 345 350				1156
gtc aaa atc acc ctc ctt tct gca tta gtg gag aca agg acc att gtg Val Lys Ile Thr Leu Leu Ser Ala Leu Val Glu Thr Arg Thr Ile Val 355 360 365				1204
cgt ttc aac agg ccc ttc ctg atg atc att gtc cct aca gac acc cag Arg Phe Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln 370 375 380				1252
aac atc ttc ttc atg agc aaa gtc acc aat ccc agc aag cct aga gct Asn Ile Phe Phe Met Ser Lys Val Thr Asn Pro Ser Lys Pro Arg Ala 385 390 395 400				1300
tgc atc aag cag tgg ggc tct cag taaggaaatt ggaatgcaag ctggatgcct Cys Ile Lys Gln Trp Gly Ser Gln 405				1354
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ctgcttatcc ttggaagggtg acagcgattc cctgtgaagc tctcacacgc acagggggccc				1474
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 <212> PRT  
 <213> Homo sapiens

<400> 16

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-5 -1 1 5

Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly  
10 15 20

Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser Leu Tyr Lys Gln Leu  
25 30 35

Val Leu Lys Ala Leu Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile  
40 45 50 55  
Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu  
60 65 70  
Thr Glu Ile Leu Lys Ala Ser Ser Ser Pro His Gly Asp Leu Leu Arg  
75 80 85  
Gln Lys Phe Thr Gln Ser Phe Gln His Leu Arg Ala Pro Ser Ile Ser  
90 95 100  
Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys  
105 110 115  
Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu  
120 125 130 135  
Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala  
140 145 150  
Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile  
155 160 165  
Thr Asp Leu Ile Lys Asp Pro Asp Ser Gln Thr Met Met Val Leu Val  
170 175 180  
Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln  
185 190 195  
Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val Met  
200 205 210 215  
Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp  
220 225 230  
Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala  
235 240 245  
Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu  
250 255 260  
Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu  
265 270 275  
Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg  
280 285 290 295  
Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala  
300 305 310  
Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu  
315 320 325  
Ala Val Ser Gln Val Val His Lys Val Val Ser Asp Val Phe Glu Glu  
330 335 340

Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser  
345 350 355

Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu  
360 365 370 375

Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys  
380 385 390

Val Thr Asn Pro Ser Lys Pro Arg Ala Cys Ile Lys Gln Trp Gly Ser  
395 400 405

Gln

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<222> (222).. (857)

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tcccaggggc ttcttttga ctggactgtc cctgctcctc cattctcctg ccaccccag 180  
acctcctcag ctccaggttg ccacotcctc tcgccagagt g atg agg tcc cgg ctt 236  
Met Arg Ser Arg Leu  
1 5  
ctg ctc tcc gtg gcc cat ctg ccc aca att ogg gag acc acg gag gag 284  
Leu Leu Ser Val Ala His Leu Pro Thr Ile Arg Glu Thr Thr Glu Glu  
10 15 20  
atg ctg ctt ggg ggt cct gga cag gag ccc cca ccc tct cct agc ctg 332  
Met Leu Leu Gly Gly Pro Gly Gln Glu Pro Pro Pro Ser Pro Ser Leu  
25 30 35  
gat gac tac gtg agg tct ata tct cga ctg gca cag ccc acc tct gtg 380  
Asp Asp Tyr Val Arg Ser Ile Ser Arg Leu Ala Gln Pro Thr Ser Val  
40 45 50  
ctg gac aag gcc acg gcc cag ggc caa ccc agg cca ccc cac agg cca 428  
Leu Asp Lys Ala Thr Ala Gln Gly Gln Pro Arg Pro Pro His Arg Pro  
55 60 65  
gcc cag gcc tgc cgg aag ggc cgc cct gct gtg tcc ctg cga gac atc 476  
Ala Gln Ala Cys Arg Lys Gly Arg Pro Ala Val Ser Leu Arg Asp Ile  
70 75 80 85  
acc gca cgt ttc agt ggc cag cag ccc aca ctg ccc atg gct gat act 524  
Thr Ala Arg Phe Ser Gly Gln Gln Pro Thr Leu Pro Met Ala Asp Thr  
90 95 100  
gtg gac ccc ctg gac tgg ctt ttt ggg gag tcc cag gaa aag cag cca 572  
Val Asp Pro Leu Asp Trp Leu Phe Gly Glu Ser Gln Glu Lys Gln Pro  
105 110 115  
agc cag agg gac ctg cca agg agg act ggc ccc tct gct ggc ctc tgg 620  
Ser Gln Arg Asp Leu Pro Arg Arg Thr Gly Pro Ser Ala Gly Leu Trp  
120 125 130  
ggt cca cat aga cag atg gac agc agc aag ccc acg ggg gcc ccc aga 668  
Gly Pro His Arg Gln Met Asp Ser Ser Lys Pro Thr Gly Ala Pro Arg  
135 140 145

ggg agg ctc tgt gaa gcc agg atg cct ggg cat tcc ctg gca aga cca 716  
 Gly Arg Leu Cys Glu Ala Arg Met Pro Gly His Ser Leu Ala Arg Pro  
 150 155 160 165  
 ccg cag gat ggg cag cag agc tct gac cta aga agc tgg act ttt ggg 764  
 Pro Gln Asp Gly Gln Gln Ser Ser Asp Leu Arg Ser Trp Thr Phe Gly  
 170 175 180  
 cag tct gcc caa gcc atg gcc tcc cgc cac cgc ccc cgc ccc agc agt 812  
 Gln Ser Ala Gln Ala Met Ala Ser Arg His Arg Pro Arg Pro Ser Ser  
 185 190 195  
 gtc ctc aga aca ctc tac tcg cac ctc ccg gtg atc cat gaa ctc 857  
 Val Leu Arg Thr Leu Tyr Ser His Leu Pro Val Ile His Glu Leu  
 200 205 210  
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 aaaaaaaaa a 2008

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 <212> PRT  
 <213> Homo sapiens

<400> 18

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Pro Ser Pro Ser Leu Asp Asp Tyr Val Arg Ser Ile Ser Arg Leu Ala  
35 40 45

Gln Pro Thr Ser Val Leu Asp Lys Ala Thr Ala Gln Gly Gln Pro Arg  
50 55 60

Pro Pro His Arg Pro Ala Gln Ala Cys Arg Lys Gly Arg Pro Ala Val  
65 70 75 80

Ser Leu Arg Asp Ile Thr Ala Arg Phe Ser Gly Gln Gln Pro Thr Leu  
85 90 95

Pro Met Ala Asp Thr Val Asp Pro Leu Asp Trp Leu Phe Gly Glu Ser  
100 105 110

Gln Glu Lys Gln Pro Ser Gln Arg Asp Leu Pro Arg Arg Thr Gly Pro  
115 120 125

Ser Ala Gly Leu Trp Gly Pro His Arg Gln Met Asp Ser Ser Lys Pro  
130 135 140

Thr Gly Ala Pro Arg Gly Arg Leu Cys Glu Ala Arg Met Pro Gly His  
145 150 155 160

Ser Leu Ala Arg Pro Pro Gln Asp Gly Gln Gln Ser Ser Asp Leu Arg  
165 170 175

Ser Trp Thr Phe Gly Gln Ser Ala Gln Ala Met Ala Ser Arg His Arg  
180 185 190

Pro Arg Pro Ser Ser Val Leu Arg Thr Leu Tyr Ser His Leu Pro Val  
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Ile His Glu Leu  
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<212> DNA  
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<222> (367).. (1068)

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cgggcaacgc cccctgctcc cggacagact cgtggcccg ctgagccct ggggctccg 180  
cagaccgcg cccgtccgc cgcagctcg gcccgcgct gccgcgtcg cggggccgc 240  
gcgggatgg ggtaggggca gcccaccga gtgggggat gggccgccct ctgggcaccg 300  
agcagcccc cgaggcctga ccaaccgcga ggaccggcgg aggagcccc cctggatgtc 360  
aagcgg atg cca agc gga tgc cac agt tcc ccc ccc agc gga ctc cgt 408  
Met Pro Ser Gly Cys His Ser Ser Pro Pro Ser Gly Leu Arg  
1 5 10  
ggg gac atg gct tgc ctg gtg ccc ctt tcc cca tat cta agc ccc acg 456  
Gly Asp Met Ala Ser Leu Val Pro Leu Ser Pro Tyr Leu Ser Pro Thr  
15 20 25 30

gtc ctc ctg ctg gtc agc tgt gac ctg ggc ttc gtg cga gca gac cgg Val Leu Leu Leu Val Ser Cys Asp Leu Gly Phe Val Arg Ala Asp Arg 35 40 45	504
cct ccc tct cct gtg aat gtg acg gtc act cac ctc aga gcc aac tcg Pro Pro Ser Pro Val Asn Val Thr Val Thr His Leu Arg Ala Asn Ser 50 55 60	552
gcc act gtg tcc tgg gac gtc cca gaa ggc aac atc gtc att ggc tac Ala Thr Val Ser Trp Asp Val Pro Glu Gly Asn Ile Val Ile Gly Tyr 65 70 75	600
tcc att tcc cag caa cgg cag aat ggc ccc ggg cag cgt gtg att cgg Ser Ile Ser Gln Gln Arg Gln Asn Gly Pro Gly Gln Arg Val Ile Arg 80 85 90	648
gag gtg aac acc acc acc cgg gcc tgt gcc ctc tgg ggc ctg gct gaa Glu Val Asn Thr Thr Thr Arg Ala Cys Ala Leu Trp Gly Leu Ala Glu 95 100 105 110	696
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agt ccc cca ggg ccc cgg gtg cac ttc cga act ctc aag ggt tct gac Ser Pro Pro Gly Pro Arg Val His Phe Arg Thr Leu Lys Gly Ser Asp 130 135 140	792
cgg cta cct tca aac agt tca agc cca ggt gac atc aca gtg gaa ggt Arg Leu Pro Ser Asn Ser Ser Ser Pro Gly Asp Ile Thr Val Glu Gly 145 150 155	840
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tat gac atc atc aag gac aat gac tcc aac aac aat ccc aag gag aag Tyr Asp Ile Ile Lys Asp Asn Asp Ser Asn Asn Asn Pro Lys Glu Lys 195 200 205	984
gga aag ggg cgg gaa cag agt cct cag gga agg cca gtg ggg aca aga Gly Lys Gly Pro Glu Gln Ser Pro Gln Gly Arg Pro Val Gly Thr Arg 210 215 220	1032
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caagatgggtg atctgcccga gactcccaga gggtaatgcc actcccacaa tctcaggcct	1198
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<213> Homo sapiens

<400> 20

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Leu Leu Val Ser Cys Asp Leu Gly Phe Val Arg Ala Asp Arg Pro Pro  
35 40 45

Ser Pro Val Asn Val Thr Val Thr His Leu Arg Ala Asn Ser Ala Thr  
50 55 60

Val Ser Trp Asp Val Pro Glu Gly Asn Ile Val Ile Gly Tyr Ser Ile  
65 70 75 80

Ser Gln Gln Arg Gln Asn Gly Pro Gly Gln Arg Val Ile Arg Glu Val  
85 90 95

Asn Thr Thr Thr Arg Ala Cys Ala Leu Trp Gly Leu Ala Glu Asp Ser  
100 105 110

Asp Tyr Thr Val Gln Val Arg Ser Ile Gly Leu Arg Gly Glu Ser Pro  
115 120 125

Pro Gly Pro Arg Val His Phe Arg Thr Leu Lys Gly Ser Asp Arg Leu  
130 135 140

Pro Ser Asn Ser Ser Ser Pro Gly Asp Ile Thr Val Glu Gly Leu Asp  
145 150 155 160

Gly Glu Arg Pro Leu Gln Thr Gly Glu Val Val Ile Ile Val Val Val  
165 170 175

Leu Leu Met Trp Ala Ala Val Ile Gly Leu Phe Cys Arg Gln Tyr Asp  
180 185 190

Ile Ile Lys Asp Asn Asp Ser Asn Asn Asn Pro Lys Glu Lys Gly Lys  
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Gly Pro Glu Gln Ser Pro Gln Gly Arg Pro Val Gly Thr Arg Gln Lys  
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Lys Ser Pro Ser Ile Asn Thr Ile Asp Val  
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<212> DNA

<213> Homo sapiens

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ttcctgagga cgtggagaaa actttctgct gagaaggaca ttttgaaggt tttgttggt	180
gaaaaagctg tttctggaat caccctaga tctttcttga agacttgaat tagattacag	240
cg atg ggg aca cag aag gtc acc cca gct ctg ata ttt gcc atc aca Met Gly Thr Gln Lys Val Thr Pro Ala Leu Ile Phe Ala Ile Thr 1 5 10 15	287
gtt gct aca atc ggc tct ttc caa ttt ggc tac aac act ggg gtc atc Val Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile 20 25 30	335
aat gct cct gag aag atc ata aag gaa ttt atc aat aaa act ttg acg Asn Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr 35 40 45	383
gac aag gga aat gcc cca ccc tct gag gtg ctg ctc acg tct ctc tgg Asp Lys Gly Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Ser Leu Trp 50 55 60	431
tcc ttg tct gtg gcc ata ttt tcc gtc ggg ggt atg atc ggc tcc ttt Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe 65 70 75	479
tcc gtc gga ctc ttc gtc aac cgc ttt ggc agg cgc aat tca atg ctg Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu 80 85 90 95	527
att gtc aac ctg ttg gct gtc act ggt ggc tgc ttt atg gga ctg tgt Ile Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys 100 105 110	575
aaa gta gct aag tcg gtt gaa atg ctg atc ctg ggt cgc ttg gtt att Lys Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile 115 120 125	623
ggc ctc ttc tgc gga ctc tgc aca ggt ttt gtg ccc atg tac att gga Gly Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly 130 135 140	671
gag atc tcg cct act gcc ctg cgg ggt gcc ttt ggc act ctc aac cag Glu Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln 145 150 155	719
ctg ggc atc gtt gtt gga att ctg gtg gcc cag atc ttt ggt ctg gaa Leu Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu 160 165 170 175	767
ttc atc ctt ggg tct gaa gag cta tgg ccg ctg cta ctg ggt ttt acc Phe Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr 180 185 190	815
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agt ccc aga ttt ttg ctc att aac aga aaa gaa gag gag aat gct aag Ser Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys 210 215 220	911
cag atc ctc cag cgg ttg tgg ggc acc cag gat gta tcc caa gac atc Gln Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile 225 230 235	959
cag gag atg aaa gat gag agt gca agg atg tca caa gaa aag caa gtc Gln Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val 240 245 250 255	1007
acc gtg cta gag ctc ttt aga gtg tcc agc tac cga cag ccc atc atc Thr Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile 260 265 270	1055
att tcc att gtg ctc cag ctc tct cag cag ctc tct ggg atc aat gct	1103



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gtg ttc tat tac tca aca gga atc ttc aag gat gca ggt gtt caa gag	1151
Val Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Glu	
290 295 300	
ccc atc tat gcc acc atc ggc gcg ggt gtg gtt aat act atc ttc act	1199
Pro Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr	
305 310 315	
gta gtt tct cta ttt ctg gtg gaa agg gca gga aga agg act ctg cat	1247
Val Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His	
320 325 330 335	
atg ata ggc ctt gga ggg atg gct ttt tgt tcc acg ctc atg act gtt	1295
Met Ile Gly Leu Lys Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val	
340 345 350	
tct ttg tta tta aag gat aac tat aat ggg atg agc ttt gtc tgt att	1343
Ser Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile	
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ggg gct atc ttg gtc ttt gta gcc ttc ttt gaa att gga cca ggc ccc	1391
Gly Ala Ile Leu Val Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro	
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Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro	
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Ala Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu	
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Val Gly Leu Leu Phe Pro Ser Ala Ala His Tyr Leu Gly Ala Tyr Val	
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Phe Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe	
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Phe Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg	
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Ala Phe Glu Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly	
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480 485 490 495	
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Val	
cctcaacaag ggagagacct catcaggatg aacccaggac gcttctgaat gctgctactt	1840
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 <212> PRT  
 <213> Homo sapiens

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Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile Asn  
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Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr Asp  
 35 40 45

Lys Gly Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Ser Leu Trp Ser

50

55

60

Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser  
65 70 75 80

Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Ile  
85 90 95

Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys Lys  
100 105 110

Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile Gly  
115 120 125

Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly Glu  
130 135 140

Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln Leu  
145 150 155 160

Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu Phe  
165 170 175

Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr Ile  
180 185 190

Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Phe Cys Pro Glu Ser  
195 200 205

Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys Gln  
210 215 220

Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile Gln  
225 230 235 240

Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val Thr  
245 250 255

Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile Ile  
260 265 270

Ser Ile Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val  
275 280 285

Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Glu Pro  
290 295 300

Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr Val  
305 310 315 320

Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Met  
325 330 335

Ile Gly Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val Ser  
340 345 350

Leu Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile Gly

355	360	365	
Ala Ile Leu Val Phe Val 370	Ala Phe Phe Glu Ile 375	Gly Pro Gly Pro Ile 380	
Pro Trp Phe Ile Val 385	Ala Glu Leu Phe Ser 390	Gln Gly Pro Arg Pro Ala 395 400	
Ala Met Ala Val 405	Ala Gly Cys Ser Asn Trp Thr 410	Ser Asn Phe Leu Val 415	
Gly Leu Leu Phe Pro Ser Ala Ala 420	His Tyr Leu Gly Ala Tyr 425 430	Val Phe	
Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe Phe 435 440 445			
Lys Val Pro Glu Thr Arg 450	Gly Arg Thr Phe Glu Asp 455 460	Ile Thr Arg Ala	
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gaa gtg cag tcc aaa atc gag aag aag tat gac gag gag ctg gag gag Glu Val Gln Ser Lys Ile Glu Lys Lys Tyr Asp Glu Glu Leu Glu Glu 15 20 25	159		
cgg ctg gtg gag tgg atc ata gtg cag tgt ggc cct gat gtg ggc cgc Arg Leu Val Glu Trp Ile Ile Val Gln Cys Gly Pro Asp Val Gly Arg 30 35 40	207		
cca gac cgt ggg ccc ttg ggc ttc cag gtg tgg ctg aag aat ggc gtg Pro Asp Arg Gly Pro Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val 45 50 55 60	255		
att ctg agc aag ctg gtg aac agc ctg tac cct gat ggc tcc aag ccg Ile Leu Ser Lys Leu Val Asn Ser Leu Tyr Pro Asp Gly Ser Lys Pro 65 70 75	303		
gtg aag gtg ccc gag aac cca ccc tcc atg gtc ttc aag cag atg gag Val Lys Val Pro Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu 80 85 90	351		
cag gtg gct cag ttc ctg aag gcg gct gag gac tct ggg gtc atc aag Gln Val Ala Gln Phe Leu Lys Ala Ala Glu Asp Ser Gly Val Ile Lys 95 100 105	399		

act gac atg ttc cag act gtt gac ctc ttt gaa ggc aaa gac atg gca 447  
 Thr Asp Met Phe Gln Thr Val Asp Leu Phe Glu Gly Lys Asp Met Ala  
 110 115 120  
 gca gtg cag agg acc ctg atg gct ttg ggc agc ttg gca gtg acc aag 495  
 Ala Val Gln Arg Thr Leu Met Ala Leu Gly Ser Leu Ala Val Thr Lys  
 125 130 135 140  
 aat gat ggg cac tac cgt gga gat ccc aac tgg ttt atg aag aaa gcg 543  
 Asn Asp Gly His Tyr Arg Gly Asp Pro Asn Trp Phe Met Lys Lys Ala  
 145 150 155  
 cag gag cat aag agg gaa ttc aca gag agc cag ctg cag gag gga aag 591  
 Gln Glu His Lys Arg Glu Phe Thr Glu Ser Gln Leu Gln Glu Gly Lys  
 160 165 170  
 cat gtc att ggc ctt cag atg ggc agc aac aga ggg gcc tcc cag gcc 639  
 His Val Ile Gly Leu Gln Met Gly Ser Asn Arg Gly Ala Ser Gln Ala  
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 ggc atg aca ggc tac gga cga cct cgg cag atc atc agt tagagcggag 688  
 Gly Met Thr Gly Tyr Gly Arg Pro Arg Gln Ile Ile Ser  
 190 195 200  
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 <212> PRT  
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<400> 24

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20 25 30

Trp Ile Ile Val Gln Cys Gly Pro Asp Val Gly Arg Pro Asp Arg Gly  
35 40 45

Pro Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val Ile Leu Ser Lys  
50 55 60

Leu Val Asn Ser Leu Tyr Pro Asp Gly Ser Lys Pro Val Lys Val Pro  
65 70 75 80

Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu Gln Val Ala Gln  
85 90 95

Phe Leu Lys Ala Ala Glu Asp Ser Gly Val Ile Lys Thr Asp Met Phe  
100 105 110

Gln Thr Val Asp Leu Phe Glu Gly Lys Asp Met Ala Ala Val Gln Arg  
115 120 125

Thr Leu Met Ala Leu Gly Ser Leu Ala Val Thr Lys Asn Asp Gly His  
130 135 140

Tyr Arg Gly Asp Pro Asn Trp Phe Met Lys Lys Ala Gln Glu His Lys  
145 150 155 160

Arg Glu Phe Thr Glu Ser Gln Leu Gln Gly Lys His Val Ile Gly  
165 170 175

Leu Gln Met Gly Ser Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly  
180 185 190

Tyr Gly Arg Pro Arg Gln Ile Ile Ser  
195 200

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<212> DNA  
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<220>  
<223> Oligonucleotide designed to act as primer for amplifying kiaa1001 gene transcript.

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<210> 26  
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<400> 26  
agccacagcc aaaaaagact tt 22

<210> 27  
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<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of kiaa1001 gene transcript.

<400> 27  
ttacatactt agagagagac tcttttagcc ag 32

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<223> Oligonucleotide designed to act as primer for amplifying asah1 gene transcript.

<400> 28  
accctaagga agttgctaac ttaaaaaa 28

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 <212> DNA  
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 <223> Oligonucleotide designed to act as primer for amplifying mgc4171 gene transcript.  
  
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 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of mgc4171 gene transcript.  
  
 <400> 33  
 tgaagagtcg gattttgaag cagc 24  
  
 <210> 34  
 <211> 24  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying lss gene transcript.  
  
 <400> 34  
 gtccgggtgc tacttgagaa acag 24

<210> 35  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying lss  
 gene transcript.  
  
 <400> 35  
 agaccccagc aatgttttcc t 21  
  
 <210> 36  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as TaqMan probe for detecting  
 amplification of lss gene transcript.  
  
 <400> 36  
 occaatggcg actggccg 18  
  
 <210> 37  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying nr0b2  
 gene transcript.  
  
 <400> 37  
 cagcacttgg ctccttagga a 21  
  
 <210> 38  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying nr0b2  
 gene transcript.  
  
 <400> 38  
 actgtgtcca aaccaaggaa gtc 23  
  
 <210> 39  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as TaqMan probe for detecting  
 amplification of nr0b2 gene transcript.  
  
 <400> 39  
 agctcttcac tcagccacac ccc 23  
  
 <210> 40  
 <211> 22  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying fabp1  
 gene transcript.  
  
 <400> 40  
 gagtttctcc ggcaagtacc aa 22



<210> 41  
 <211> 20  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying fabp1 gene transcript.  
  
 <400> 41  
 cagaccgatt gccttcatga 20  
  
 <210> 42  
 <211> 25  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of fabp1 gene transcript.  
  
 <400> 42  
 tgcagagcca ggaaaacttt gaagc 25  
  
 <210> 43  
 <211> 22  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying hpn gene transcript.  
  
 <400> 43  
 gaaaccagat caagccaag at 22  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying hpn gene transcript.  
  
 <400> 44  
 ccctggcagg catcaatg 18  
  
 <210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of hpn gene transcript.  
  
 <400> 45  
 ttctgtgctg gctacccga 20  
  
 <210> 46  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying serpin3 gene transcript.

<400> 46  
gaggaggga cagaagcatc t 21

<210> 47  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying serpina3 gene transcript.

<400> 47  
ccttgctcc actaatgcag aaag 24

<210> 48  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of serpina3 gene transcript.

<400> 48  
tgccacagca gtcaaatca ccct 24

<210> 49  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying depp gene transcript.

<400> 49  
tgtgtggca ttgggagagt 20

<210> 50  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying depp gene transcript.

<400> 50  
tgtagcact gagtgtaca gattc 25

<210> 51  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of depp gene transcript.

<400> 51  
cccccattgat gagggccaag at 22

<210> 52  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying flj22362

gene transcript.

<400> 52  
ggtaatgccca ctcccacaat ct 22

<210> 53  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying flj22362  
gene transcript.

<400> 53  
ccttctggct ctgctcacag t 21

<210> 54  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as TaqMan probe for detecting  
amplification of flj22362 gene transcript.

<400> 54  
aggcctggta cccatcctct ttc 23

<210> 55  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying slc2a3  
gene transcript.

<400> 55  
gcttgaaaag gtgaccttgc a 21

<210> 56  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as primer for amplifying slc2a3  
gene transcript.

<400> 56  
tgccttactg ccaacctact gtt 23

<210> 57  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> Oligonucleotide designed to act as TaqMan probe for detecting  
amplification of slc2a3 gene transcript.

<400> 57  
tcatgtcaac tttctggctc etc 23

<210> 58  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
 <223> Oligonucleotide designed to act as primer for amplifying tagln  
 gene transcript.  
 <400> 58  
 gagcataaga gggaattcac agaga 25  
 <210> 59  
 <211> 20  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> Oligonucleotide designed to act as primer for amplifying tagln  
 gene transcript.  
 <400> 59  
 ctgttgctgc ccatctgaag 20  
 <210> 60  
 <211> 27  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> Oligonucleotide designed to act as TaqMan probe for detecting  
 amplification of tagln gene transcript.  
 <400> 60  
 agctgcagga gggaaagcat gtcattg 27